

SEQUENCE LISTING

<110> Bolton, Alexandra J.
Perez-Casal, Jose
Fontaine, Michael
Potter, Andrew A.

<120> IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
STREPTOCOCCUS INFECTION

<130> 9000-0055

<140>

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<160> 12

<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer gapC1

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37

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer gapC1r

<400> 2

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35

<210> 3

<211> 1011

<212> DNA

<213> Streptococcus dysgalactiae

<220>

<221> CDS

<222> (1)..(1011)

<400> 3

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gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc	96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile	
20 25 30	
aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tac gat	144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp	
35 40 45	
aca act caa gga cgt ttt gac gga act gtt gaa gtt aaa gaa ggt gga	192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly	
50 55 60	
ttt gaa gta aac gga aac ttc atc aaa gtt tct gct gaa cgt gat cca	240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro	
65 70 75 80	
gaa aac atc gac tgg gca act gac ggt gtt gaa atc gtt ctg gaa gca	288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala	
85 90 95	
act ggt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct	336
Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala	
100 105 110	
aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
aaa aca gtt gtt ttc aac act aac cac gac att ctt gac ggt act gaa	432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cct atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct ctt cac gat gca ttt ggt atc caa aaa ggt ctt atg act	528
Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr	
165 170 175	
aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	

cct aac tca act ggt gct gct aaa gct atc ggt ctt gtt atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
ttg aat ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tct gtt	768
Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val	
245 250 255	
gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt	816
Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly	
260 265 270	
tac act gaa gat cca att gtt tct tca gat atc gta ggc gtg tca tac	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr	
275 280 285	
ggt tca ttg ttt gac gca act caa act aaa gtt atg gaa gtt gac gga	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly	
290 295 300	
tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac	960
Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gct caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

<210> 4
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 <212> PRT
 <213> Streptococcus dysgalactiae

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 35 40 45
 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
 50 55 60

Phe	Glu	Val	Asn	Gly	Asn	Phe	Ile	Lys	Val	Ser	Ala	Glu	Arg	Asp	Pro	
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Gly	Ser	Val	Thr	Glu	Leu	Val	Val	Thr	Leu	Asp	Lys	Asn	Val	Ser	Val	
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Asp	Glu	Ile	Asn	Ala	Ala	Met	Lys	Ala	Ala	Ser	Asn	Asp	Ser	Phe	Gly	
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Tyr	Thr	Glu	Asp	Pro	Ile	Val	Ser	Ser	Asp	Ile	Val	Gly	Val	Ser	Tyr	
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Gly	Ser	Leu	Phe	Asp	Ala	Thr	Gln	Thr	Lys	Val	Met	Glu	Val	Asp	Gly	
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Ser	Gln	Leu	Val	Lys	Val	Val	Ser	Trp	Tyr	Asp	Asn	Glu	Met	Ser	Tyr	
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<212> DNA

<213> Streptococcus agalactiae

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<221> CDS

<222> (1)..(1011)

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gca ttc cgt cgc atc caa aac gta gaa ggt gtt gaa gtt act cgt atc 96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac 144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

aca act caa ggt cgt ttc gac ggt act gtt gaa gtt aaa gaa ggt gga 192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
50 55 60

ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca 240
Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
65 70 75 80

gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca 288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95

act ggt ttc ttt gca tca aaa gaa aaa gct gga caa cac atc cat gaa 336
Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu
100 105 110

aat ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt 384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
115 120 125

aaa aca gtt gtt ttc aac act aac cac gat atc ctt gat gga act gaa 432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

aca gtt atc tca ggt gct tca tgt act aca aac tgt ctt gct cca atg 480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

gct aaa gct tta caa gac aac ttt ggt gtt aaa caa ggt ttg atg act 528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175

act atc cac gca tac act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cggt ggt ggt gac ctt cggt cggt gct cggt gca ggt gct gca aac atc gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val	
195 200 205	
cct aac tca act ggt gct gca aaa gct atc gga ctt gtt atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
ttg aac ggt aaa ctt gat ggt gct gca caa cggt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gaa ttg gtt gca act ctt gaa aaa gac gta act gtc	768
Gly Ser Val Thr Glu Leu Val Ala Thr Leu Glu Lys Asp Val Thr Val	
245 250 255	
gaa gaa gta aat gca gct atg aaa gca gca gct aac gat tca tac ggt	816
Glu Glu Val Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
tat act gaa gat cca atc gta tca tct gat atc gtt ggt att tca tac	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr	
275 280 285	
ggt tca ttg ttt gat gct act caa act aaa gtt caa act gtt gac ggt	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
290 295 300	
aac caa ttg gtt aaa gtt gtt tca tgg tac gat aac gaa atg tca tac	960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act tca caa ctt gtt cggt aca ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ser Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

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<212> PRT

<213> Streptococcus agalactiae

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Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
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<210> 7

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<213> Streptococcus uberis

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<222> (1)..(1011)

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gca ttc cgt cgt att caa aac gtt gaa ggt gtt gaa gta act cgt att 96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

aac gat ctt act gac cca aat atg ctt gca cac ttg ttg aaa tat gat 144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

aca act caa ggt cgt ttc gac ggt aca gtt gaa gtt aaa gat ggt gga 192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60

ttc gaa gtt aac gga aac ttc atc aaa gtt tct gct gaa aaa gat cca 240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
65 70 75 80

gaa aac att gac tgg gca act gac ggt gta gaa atc gtt ctt gaa gca 288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95

act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gct 336
Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Ala
100 105 110

aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga gat gat gtt 384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
115 120 125

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Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

act gta att tca ggt gct tca tgt act act aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct ttg caa gat aac ttt ggt gtt aaa caa ggt ttg atg aca	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
act atc cac gct tac act ggt gac caa atg atc ctt gac gga cca cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gca agc aac att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val	
195 200 205	
cct aac tca act ggt gct gct aaa gca atc ggt ctt gta atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
210 215 220	
tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gaa tta gta gca gtt ctt gaa aaa gaa act tca gtt	768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Glu Thr Ser Val	
245 250 255	
gaa gaa atc aac gca gca atg aaa gca gct gca aac gat tca tac gga	816
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
tac act gaa gac cca atc gta tct tct gat atc atc ggt atg gct tac	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr	
275 280 285	
ggg tca ttg ttt gat gct act caa act aaa gta caa act gtt gat gga	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
290 295 300	
aat caa tta gtt aaa gtt gtt tca tgg tat gac aac gaa atg tct tac	960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gca caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

<210> 8

<211> 336

<212> PRT

<213> Streptococcus uberis

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35 40 45
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
65 70 75 80
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95
Thr Gly Phe Phe Ala Lys Lys Ala Ala Glu Lys His Leu His Ala
100 105 110
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
115 120 125
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
180 185 190
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val
195 200 205
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
210 215 220
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225 230 235 240
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Glu Thr Ser Val
245 250 255
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
260 265 270

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr
275 280 285

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
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Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
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gct ttc cgt cgt att caa aat gta gaa ggt gtt gaa gtt act cgc atc 96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

aac gac ctt aca gat cca aat atg ctt gca cac ttg tta aaa tac gat 144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

aca act caa ggt cgt ttt gac ggt act gta gaa gtt aaa gat ggt gga 192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60

ttt gac gtt aac gga aaa ttc att aaa gtt tct gct gaa aaa gat cca 240
Phe Asp Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
65 70 75 80

gaa caa att gac tgg gca act gac ggt gtt gaa atc gtt ctt gaa gca 288
Glu Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95

act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gaa 336
Thr Gly Phe Phe Ala Lys Lys Ala Ala Glu Lys His Leu His Glu
100 105 110

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Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
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Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt att tca ggt gct tca tgt act aca aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gct tta caa gat aac ttt ggc gta aaa caa ggt tta atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
165 170 175	
aca atc cac gct tac act ggt gat caa atg ctt ctt gat gga cct cac	576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Leu Leu Asp Gly Pro His	
180 185 190	
cgt ggt ggt gac tta cgt cgt gcc cgt gct ggt gct aac aat att gtt	624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Asn Asn Ile Val	
195 200 205	
cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cct gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
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tta aat ggt aaa ctt gac ggt gct gca caa cgt gta cca gtt cca aca	720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
ggt tca gta aca gaa tta gta gca gtt ctt aat aaa gaa act tca gta	768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Asn Lys Glu Thr Ser Val	
245 250 255	
gaa gaa att aac tca gta atg aaa gct gca gct aat gat tca tat ggt	816
Glu Glu Ile Asn Ser Val Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
tac act gaa gat cca atc gta tca tct gat atc gtt ggt atg tct ttc	864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe	
275 280 285	
ggt tca tta ttc gat gct act caa act aaa gta caa act gtt gat gga	912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
290 295 300	
aat caa tta gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac	960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
305 310 315 320	
act gct caa ctt gat cgt aca ctt gag tac ttt gca aaa atc gct aaa	1008
Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys	
325 330 335	
taa	1011

<210> 10
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<400> 10

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			180					185					190		
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		195					200					205			
Pro	Asn	Ser	Thr	Gly	Ala	Ala	Lys	Ala	Ile	Gly	Leu	Val	Ile	Pro	Glu
	210					215					220				
Leu	Asn	Gly	Lys	Leu	Asp	Gly	Ala	Ala	Gln	Arg	Val	Pro	Val	Pro	Thr
225					230				235						240
Gly	Ser	Val	Thr	Glu	Leu	Val	Ala	Val	Leu	Asn	Lys	Glu	Thr	Ser	Val
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 Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe
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 Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
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 Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
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 aat gac ctt aca gat cct aac atg ctt gca cac ttg ttg aaa tat gat 144
 Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
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 Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
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 Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
 65 70 75 80
 gca aac att gac tgg gct act gat ggt gta gac atc gtt ctt gaa gca 288
 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
 85 90 95
 aca ggt ttc ttc gct tct aaa gca gct gct gaa caa cac att cac gct 336
 Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
 100 105 110

aac ggt gcg aaa aaa gtt gtt atc aca gct cct ggt gga aat gac gtt	384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val	
115 120 125	
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Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu	
130 135 140	
aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cca atg	480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met	
145 150 155 160	
gct aaa gca tta caa gat aac ttt ggt gta aaa caa ggt tta atg act	528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr	
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Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His	
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Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Asn Ile Val	
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cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cca gaa	672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu	
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Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr	
225 230 235 240	
gga tca gta act gaa tta gta gca gtt ctt gaa aaa gat act tca gta	768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val	
245 250 255	
gaa gaa atc aat gca gct atg aaa gca gca gct aac gat tca tac ggt	816
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly	
260 265 270	
tac act gaa gat gct atc gta tca tca gat atc gta ggt att tct tac	864
Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr	
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Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly	
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Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr	
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 50 55 60
 Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
 65 70 75 80
 Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
 85 90 95
 Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
 100 105 110
 Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
 115 120 125
 Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
 130 135 140
 Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
 145 150 155 160
 Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
 165 170 175
 Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His
 180 185 190
 Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Ala Asn Ile Val
 195 200 205

